

09607669-100101

Signal
peptide

AS
homology
region

1	atggatgtggcgccgctgcgttgccctgctttttagctctctggcttctgtacccgtgg	60
1	[M D V A A A A L P A F V A L W L L Y P W	20
61	cctctcctggggcgcccttggCcagttctcagcaggtggctgtacttttgatgatggg	120
21	P L L G S] A L G Q F S A [G G C T F D D G	40
121	ccaggggcttgtgactaccaccaggatttatacgaatgactttgagtggggtccatgtcagt	180
41	P G A C D Y H Q D L Y D D F E W V H V S	60
181	gcgaggaacctcattacctgccccCgaaatgcctcaaggttcctatatggttgGac	240
61	A Q E P H Y L P P E M P Q G S Y M V V D	80
241	tcctcaaatacatgatcctggagaaaaagccagacttcagctgcctaccatgaaggagaat	300
81	S S N H D P G E K A R L Q L P T M K E N	100
301	gacaccactgcattgatttcagttacctggttatatagccagaaggggtgaaccctggc	360
101	D T H C I D F S Y L L Y S Q K G L N P G	120
361	actttgaatacctagttaggggtgaataaaggacctcttgctaataccaatttgaatgta	420
121	T L N I L V R V N K G P L A N P I W N V	140
421	actggattcactggctgattggcttcgggctgaactagctgtgagcaccttttggccc	480
141	T G F T G R D W L R A E L A V S T F W P	160
481	aatgaataccaggtaatatttgaagctgaagtctcaggaggagaagtggttatattgcc	540
161	N E Y Q V I F E A E V S G G R S G Y I A	180
541	attgatgacatccaagtcctgagttatccttgcgataaatctcctcattttctccgctt	600
181	I D D I Q V L S Y] P C D K S P H F L R L	200
601	ggtgatgtggaggtcaatgctgggcagaatGctacatttcagtgcatgtacagggaga	660
201	G D V E V N A G Q N A T F Q C I A T G R	220
661	gatGCTgTGcataacaagttatggctgcagagacgcaatggagaagacatacccgtagcc	720
221	D A V H N K L W L Q R R N G E D I P V A	240
721	cagactaagaacataaatcacagaagatttgctgcctctttcagattgcaagaagtgaca	780
241	Q T K N I N H R R F A A S F R L Q E V T	260
781	aaaactgaccaggatttgtaccgctgcgtaactcagtcagaacgaggttctggggtttcc	840
261	K T D Q D L Y R C V T Q S E R G S G V S	280

FIG. 1(1)

841	aattttgctcaactcattgtgagagaaccacctagaccattgctcctcccagctgctt	900
281	N F A Q L I V R E P P R P I A P P Q L L	300
901	ggtgttggcctacttacttctgctgatccaactaaatgccaactctattattggcgatggc	960
301	G V G P T Y L L I Q L N A N S I I G D G	320
961	cccatcatcctgaaagaagtagagtatcgatgacatcaggatcttggacagaaacccat	1020
321	P I I L K E V E Y R M T S G S W T E T H	340
1021	gcagtcaacgcaccaacatataagttgtggcatttagaccagatacagaatacagagatc	1080
341	A V N A P T Y K L W H L D P D T E Y E I	360
1081	cgctgctgcttaccagacctggcgaagggggaactgggctgccaggaccaccactgatc	1140
361	R V L L T R P G E G G T G L P G P P L I	380
1141	actagaacgaagtgtgcagaacctatgctggacaccaaagactttaagattgctgaaatc	1200
381	T R T K C A E P M R T P K T L K I A E I	400
1201	caggcaaggcgcttgcagtgactgggagtccttgggctacaacatcactcgttgccac	1260
401	Q A R R I A V D W E S L G Y N I T R C H	420
1261	actttcaacgtcactatctgctaccattacttccgtggccacaatgagagcagggcagac	1320
421	T F N V T I C Y H Y F R G H N E S R A D	440
1321	tgcttggacatggaccccaaagcccctcagcatgttgtgaaccatctgccaccttacaca	1380
441	C L D M D P K A P Q H V V N H L P P Y T	460
1381	aatgtcagcctcaagatgatcctaaccaaccagagggaagggaaggagagcgaagagaca	1440
461	N V S L K M I L T N P E G R K E S E E T	480
1441	atcatccaaactgatgaagatgtgccgggctgtgccagtcaaatccctccaaggaaca	1500
481	I I Q T D E D V P G P V P V K S L Q G T	500
1501	tcctttgaaaacaagatcttctgaactggaaagagccactggaaccgaatggaattatc	1560
501	S F E N K I F L N W K E P L E P N G I I	520
1561	actcagtatgaggtgagctatagcagcataagatcatttgaccctgctgttccagtggct	1620
521	T Q Y E V S Y S S I R S F D P A V P V A	540
1621	gggccccacagactgtatcaaatttatggaatagtacacaccatgtatttatgcatctt	1680
541	G P P Q T V S N L W N S T H H V F M H L	560
1681	caccctggaaccacctaccagttttttataagagccagCactgtcaaaggctttggacca	1740
561	H P G T T Y Q F F I R A S T V K G F G P	580

FIG. 1(2)

Trans-
membrane

1741	gcaacagccatcaatgtgaccacaaatatctcagctccaagcttacctgactatgaagga	1800
581	A T A I N V T T N I S A P S L P D Y E G	600
1801	gttgatgcctctctgaatgaaactgccaccaccatcacagtactattgaggcctgcacaa	1860
601	V D A S L N E T A T T I T V L L R P A Q	620
1861	gccaaaggtgctcctatcagtgcttatcaaattgtgtggagcagctacaccacatcga	1920
621	A K G A P I S A Y Q I V V E Q L H P H R	640
1921	acgaagcgtgaagcaggggccatggaatgctaccaggtaccggttacataccagaacgcc	1980
641	T K R E A G A M E C Y Q V P V T Y Q N A	660
1981	ctaagtggggGcgcgCcttattactttgccgcagaacttccccctgggaatcttcccag	2040
661	L S G G A P Y Y F A A E L P P G N L P E	680
2041	cctgtcccttcaccggtgggtgacaaccggacctataaaggccttttggaaacctcccctg	2100
681	P A P F T V G D N R T Y K G F W N P P L	700
2101	gccccccgcaaaggatacaacatctatttccaagcgatgagcagtggtggagaaggaaact	2160
701	A P R K G Y N I Y F Q A M S S V E K E T	720
2161	aaaacccaatgtgtacgaattgctacaaaagcagcagcaacAgaagaaccagaagtgatc	2220
721	K T Q C V R I A T K A A A T E E P E V I	740
2221	ccagaccgggcaaaGCagacagacagagtggtgaaaatcgcgggCatcagtgctggcatc	2280
741	P D P A K Q T D R V V K I A G I S A G I	760
2281	ctagtgttcattccttctcctgtgtgtgtcatagtaattgtgaaaaagagcaagcttgct	2340
761	L V F I L L L L V V I V I V I K K S K L A	780
2341	aagaagcgcaaagatgcaatggggaacacacgtcaggagatgaccacatggtgaatgct	2400
781	K K R K D A M G N T R Q E M T H M V N A	800
2401	atggaccgaagttatgctgaccagagcaccctgcatgcagaagacccctttccctcacc	2460
801	M D R S Y A D Q S T L H A E D P L S L T	820
2461	ttcaTggaccaacataacttcagtcgaagattgcccaatgatccacttggtgacgactgcc	2520
821	F M D Q H N F S P R L P N D P L V P T A	840
2521	gtgttagatgagaaccacagtgccacagcagagtcagtcgtctCctggatgttcctcga	2580
841	V L D E N H S A T A E S S R L L D V P R	860

FIG. 1(3)

PTPase
Domain I

2581	tacctctgcgaaggacagagtccttctatcagacaggacagctgcacccagccatcagg	2640
861	Y L C E G T E S P Y Q T G Q L H P A I R	880
2641	gtggccgacttactgcagcacattaacctcatgaagacatcagacagctatgggttcaaa	2700
881	V A D L L Q H I N L M K T S D S Y G F K	900
2701	gaggaatacagagagCttctttgaaggccagtcagcctcttgggatgtggctaaaaaggat	2760
901	E E Y E S F F E G Q S A S W D V A K K D	920
2761	caaacagagcaaaagaaccgatacggaaacattatcgcatatgatcactccagagtcac	2820
921	Q N R A K [N R Y G N I I A Y D H S R V I	940
2821	ctgcaacctgtggaagatgaccttcttcagattacattaatgccaactacatcgacatt	2880
941	L Q P V E D D P S S D Y I N A N Y I D I	960
2881	tggctgtacagggatggctaccagagaccaagccactacattGCaactcaaggccagtt	2940
961	W L Y R D G Y Q R P S H Y I A T Q G P V	980
2941	catgaaaccgtatatgatttttGGAggatgggtgtggcaagagcagtcctgcctgtattgtg	3000
981	H E T V Y D F W R M V W Q E Q S A C I V	1000
3001	atggctcactaaTtttagtgGaagtTGGCCGggtgaaatgctataaatattggcctgatgat	3060
1001	M V T N L V E V G R V K C Y K Y W P D D	1020
3061	actgaggtttatgggtgacttcaaagtcaCTGCgtagaaatggagccacttgctgagtat	3120
1021	T E V Y G D F K V T C V E M E P L A E Y	1040
3121	gtcgttaggacattcaccttggaaaggaggggctataatgaaatccgtgaagtcaaacag	3180
1041	V V R T F T L E R R G Y N E I R E V K Q	1060
3181	ttccacttcactggctggcctgaccatgggtgtccataaccacgcaacagggctcctgtca	3240
1061	F H F T G W P D H G V P Y H A T G L L S	1080
3241	tttatccggagagtcgaagctatctaaccctcccagtgctgggcccattgtcgtacactgc	3300
1081	F I R R V K L S N P P S A G P I V V H C	1100
3301	agtgtggtgtcgtggcgacagcgtgttacattgttattgacataatgtggacatggct	3360
1101	S A G A G R T G C Y I V I D I M L D M A	1120
3361	gaaagagaggggtgtgggtgacatctacaactgtgtgaaagccttacgatctcggcgcatt	3420
1121	E R E G V V D I Y N C V K A L R S R R I	1140
3421	aatatggtacagacagaggaacagtacatttttattcatgatgccatttttagaagcctgc	3480
1141	N M V Q T E E Q Y I F I H D A I L E] A C	1160

FIG. 1(4)

PTPase
Domain II

3481	ttatgtggagaaactgccatccctgtgtgtgaatttaaagctgcatatttgatatgatt	3540
1161	L C G E T A I P V C E F K A A Y F D M I	1180
3541	cgaatagactctcagactaactcctctcatctcaaagatgaatttcagactctgaattcg	3600
1181	R I D S Q T N S S H L K D E F Q T L N S	1200
3601	gtcaccctcgactacaagctgaagactgcagcatagcctgcctgccaaggaacctgac	3660
1201	V T P R L Q A E D C S I A C L P R [N H D	1220
3661	aagaaccgtttcatggatgtgctccacctgacagatgtctgccttttttaattacaatt	3720
1221	K N R F M D M L P P D R C L P F L I T I	1240
3721	gatggggagagCagtaactacatcaatgctgctcttatggatagctataggcagccagca	3780
1241	D G E S S N Y I N A A L M D S Y R Q P A	1260
3781	gctttcatcgtCacacaataccactgccaacactgtgaaagacttCtggagattagta	3840
1261	A F I V T Q Y P L P N T V K D F W R L V	1280
3841	tatgattAcggatgtacctccatcgtgatgctaaatgaagtggacctgtctcagggctgc	3900
1281	Y D Y G C T S I V M L N E V D L S Q G C	1300
3901	ccacagtactggccagaagaaggaatgctgcatatggctcctatccaagtgggaatgtatg	3960
1301	P Q Y W P E E G M L R Y G P I Q V E C M	1320
3961	tcttgttcaatggactgtgatgtgatcaatcgaatttttagaatatgcaacctaacgaga	4020
1321	S C S M D C D V I N R I F R I C N L T R	1340
4021	ccacaggagggctatctgatgtgtacaacagTTCagtacctaggctgggcttctcatcga	4080
1341	P Q E G Y L M V Q Q F Q Y L G W A S H R	1360
4081	gaagtgcctggctccaaacgctcgtttttgaaattgatactgCaggtggaaaaatggcaa	4140
1361	E V P G S K R S F L K L I L Q V E K W Q	1380
4141	gaggaatgtgaagaaggggaaggccggaacaatcatccactgcttgaatggcgggtgggCGC	4200
1381	E E C E E G E G R T I I H C L N G G G R	1400
4201	agtggcatgttctgtgccataggcattgtgtgtggagatgggtgaagcggcaaatgtggtg	4260
1401	S G M F C A I G I V V E M V K R Q N V V	1420
4261	gatgttttccatgcagtaaaagacgctgaggaacagcaagccaaacatgggtggaagcccg	4320
1421	D V F H A V K T L R N S K P N M V E A P	1440
4321	gagcagtatcgTttttgctatgatgtggcgtagagtacctggagtcctcatag	4374
1441	E Q Y R F C Y D V A L E Y L E] S S *	1458

FIG. 1(5)

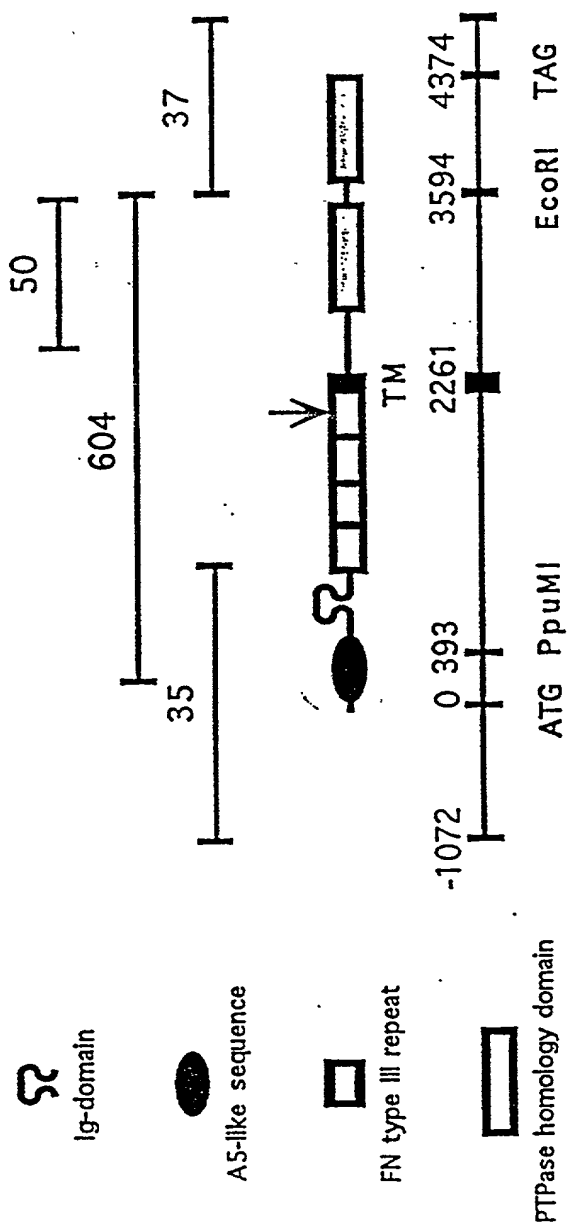


FIG. 2

	A5	IG	FN-III (x4)	TH	PTP-1	PTP-2																			
1	H D V A A A L P A F V A L W L L Y P P H Y L P P E H P Q G S A L G Q Q F S A G G C T F D D G P G A C D Y H Q D L	Y D D F E W V H V S A Q E P H Y L P P E H P Q G S A L G Q Q F S A G G C T F D D G P G A C D Y H Q D L	D T H C I D F S Y L L Y S Q K G L N P P G T L N G I L V R V V D S S N H D P P G E K A R L Q L T P T R M K E N	E E L A V S T F W P N A T F Q Q C I A T G R D A V X N K G L O R R N Q X D I P V A Q T K N I N R R R J	A A S F R L Q X V T K T D Q D Z Y R C V T Q S E R G S G V S N F A Q Q L I V R E P P A V N A P T Y A P P Q L L W	G V G P T Y L L I Q L N A N S I I G D G P I I L K K E V E Y R M T S G S W T E P H A V N A P T Y A P P Q L L W	H L D R P P I A V D W E S L G Y N I T R G E G T F N V T I C Y H Y T R R G H N E S R A D C L D M D P P K A A P Q	Q A R R P I A V D W E S L G Y N I T R G E G T F N V T I C Y H Y T R R G H N E S R A D C L D M D P P K A A P Q	S F E N K I F L N W K E P L E P N G I I T Q Y E V S Y S S I R S F D P A V P V A G P P Q T V S N L W	N S T H H V F M H L H P G T T Y Q F I I R A S T V K K G F G P A T A I N V T H R T Y K K E A F G A N P P L	V D A S L N E T A T T I T V L R P P A Q A E L P G R I A T K A A A P T E E P E V I P D P A K Q T D R V	Y Q P K G Y N I A F Q A H S S V E K E T K T Q C V R I A T K A A A P T E E P E V I P D P A K Q T D R V	V K I A G I S A G I L V F I L L L V I V I V K K S K L A K K R K D A M G N T R Q E M T H M V N A	M D R S Y A D Q S T L H A E D P L S L T F M D Q H N F S P R L P N D P L V P T A L M K T S D S Y G F K	E E S Y E S F F E G Q S A S W D V A K K D Q N R A K N R Y G N I I A Y D H S R V I L Q P V E D D P S S	D Y I H A N Y I D I W L Y R D G Y Q R P S H Y I A T Q G P V H E T V Y D F W R R M V V Q E Q S A C I V	M V T N L V E V G R V K C Y K Y W P D D T E V Y G D F K V T C V E H E P L A E Y V P S A T F T L V E R R C	G Y H E I R E V K Q F H F T G W P D H G A E R E G V D I Y N C V K A L R S R R I N M V Q T E E Q Y I	F I H D A I L E A C I L V D I H L D H A E R E G V D I Y N C V K A L R S R R I N M V Q T E E Q Y I	V T P R L Q A E D C S I A C L P R N H D K N R F H D H L P P D R C L P F F L I T I D G E S S N Y I N A	A L M D S Y R Q P A A F I V T Q Y P L P N T V K K D F W R L V Y D Y G C C T S I V M L N E E G V L M V Q Q R	P Q Y W P E E G H L R Y G P I Q V E C H S C S H D C D V E K K W Q R E I F R E E G E G R T I I H C L N G V G Q	F Q Y L G W A S H R E V P G S K R S F L K K I L Q V E K K W Q R E I F R E E G E G R T I I H C L N G V G Q	S G M F C A I G I V V E H V K R Q N V D V F H A V K T L R R N S K P N H V E A P E O Y R F C Y D V A	L E Y L E S .

I (296) * P Q L L G V G P T Y L L I Q L N A N S I I G D G P I I L K E V E Y R M T S G S W T E T H A V N A P T Y K L W H L D P D T E . Y E I R V L L T R P G E G G T G L P G P P L I T R T *
 II (392) P . K T L K I A E I Q A . . R R I A V D W E S L G Y N I T R C H T F N V T I C Y H Y F R G H N E S R A D C L D M D P K A . . . P Q H V V N H L P P Y T N V S L K M I L . T N P E G
 III (493) P V K S L Q G T S F E . . . N K I F L N W K E P L E P N G I I T Q Y E V S Y S S I R S F D P A V P V A G P P Q T V S N L M N S T H H V F M H L H P G T T Y Q F F I R A S T V K G F
 IV (596) P D Y E G V D A S I N E T A T T I T V L L R P A Q A K A P I S A Y Q I V V E Q L H P H R T K R . E A G A M E C Y Q V P V T Y Q N A L S G G A P Y Y F A A E L P P G N L P
 F B N - I I I (7) P P T N L H L E A N P D T . G V L T V S W E R S T T P D . . I T G Y R I T T T P N G Q Q G N S L E E V W H A D Q S S C T F D N L S P G L E Y N V S V Y . . T V K O D

FIG. 4

PTP-X (34)	GGCTFDDGPGACDYHQDLYDDFEWVHVSQAE.PHYLPPEMPQGSYMWVDSSNHDPEKARLQLPTMKEN.DTHCIDFSYLLYSQK
PTP-μ (26)	GGCLFDEPYSTCGYSQADEDDFNWEQVNTLTPT.SDPWMPSGSFMVNTSGKPEQRAHLLLPQLKEN.DTHCIDFHYFVSSKS
A5 (651)	CKFGWSQKTVCNWQHDISSDLKWAVLNSKTGP.VQDHTGDGNFIYSEADERHEGRAARLMSPVVSSSRSAHCLTFWYHM...D
Consensus	-----C-----D---D---W---N---T-P-----G-F-----E---ARL---P-----HC---F-Y-----

PTP-X	GLNPCTLNILVRVN.KGPLANPIWNVGTGTRDWLRAELAVSTFWPNEYQVIFEAFVSGRSGYIAIDDIQVLSY
PTP-μ	NAAPGLLNIVYKVN.NGPLCNPIWNISGDPTRTWRAELAISTFWPNFYQVIFEV.VTSGHQGYLAIDVKVLGH
A5	GSHVGTLSIKLYEMEEEDFDQTLWTVSGNQGDQWKEARVVLHKTMKQ.YQVIVEC ^W VGKGSAGGIADVDDIIIANH
Consensus	G---CTL-I--K-----W-VSG--G--W--A-----YQVI-E--V--G--G-IA-DDI-----H

FIG. 5

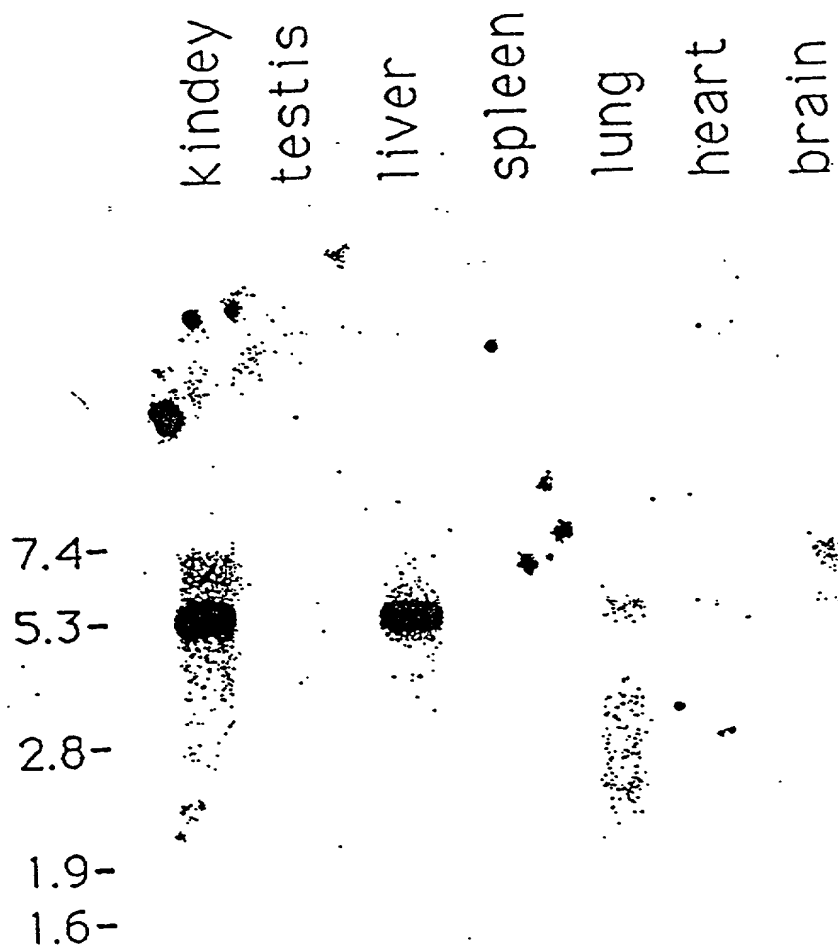


FIG. 6

09887569-100301

Transfected:	-	-	-	+	+	+
Antibody:	pre	α - κ	α - κ	pre	α - κ	α - κ
Peptide:	-	-	+	-	-	+

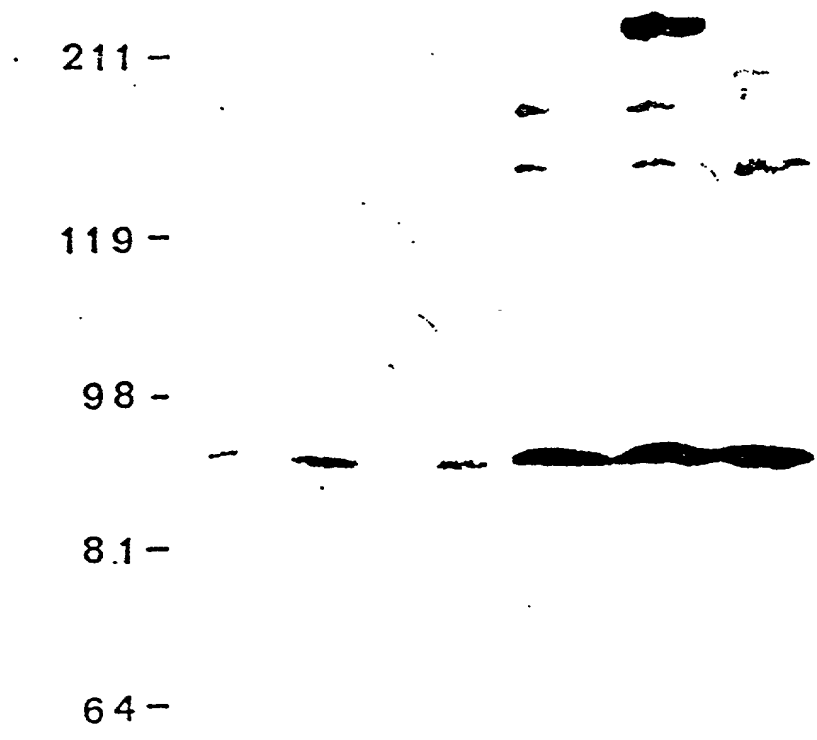


FIG. 7

Treatment	[³² P]PO ₄ Released (% of total input)
Control	22
100 mg/kg	50
200 mg/kg	30
400 mg/kg	90
800 mg/kg	24

FIG. 8

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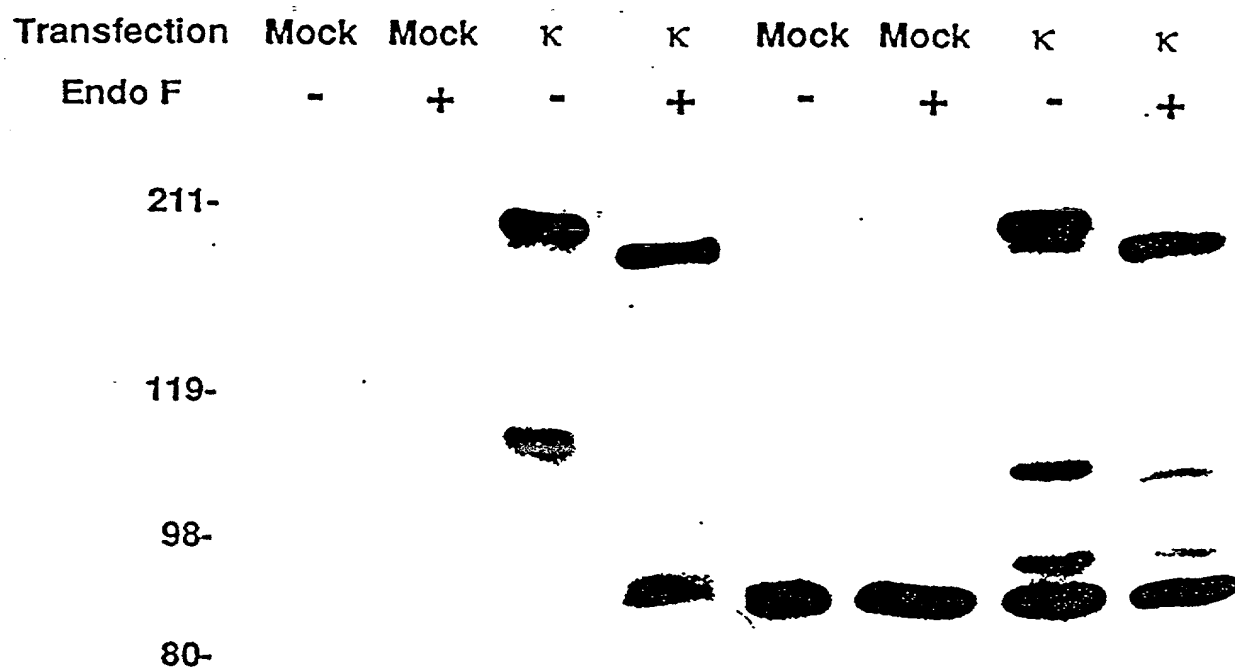


FIG. 9

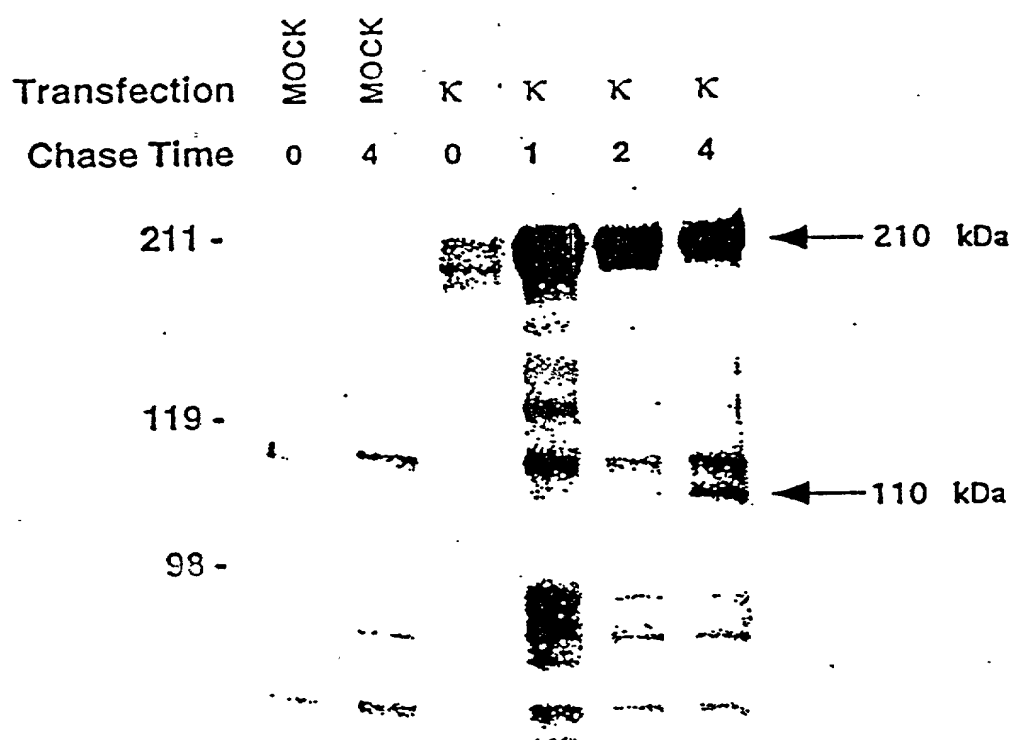


FIG. 10

09067569:100101

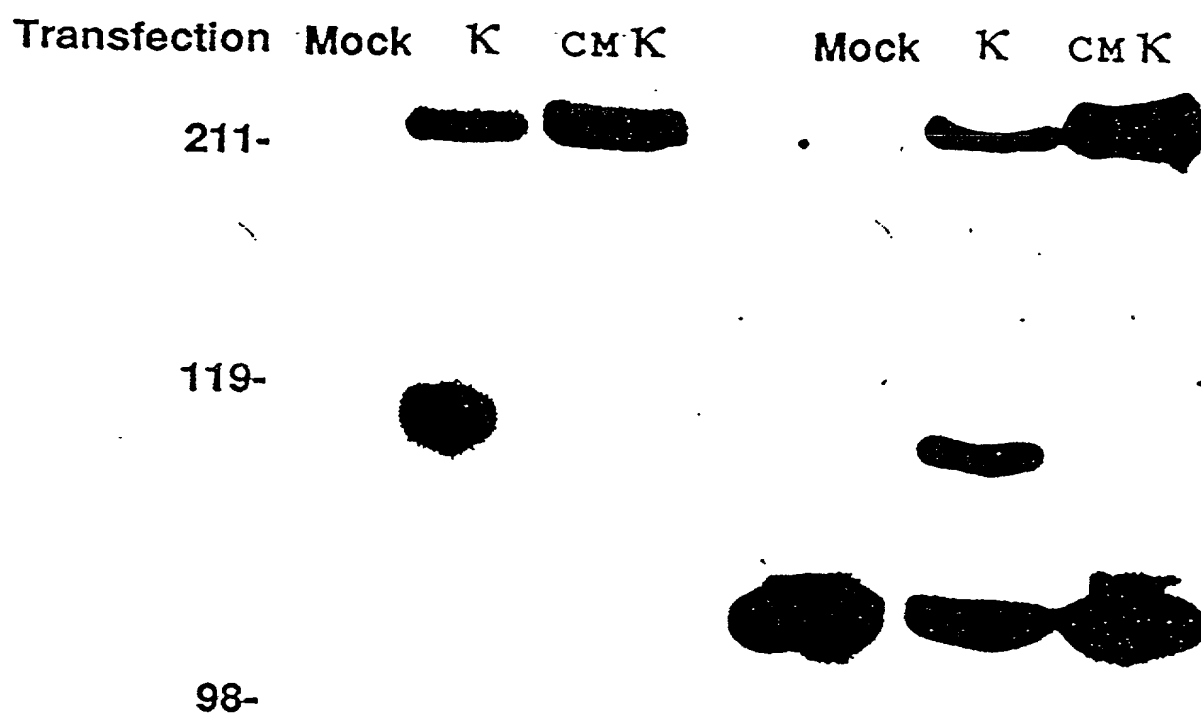


FIG. 11

09887669.100101

Transfection	Mock	K	K
IP	116	116	Total lysate

211-



119-



98-



FIG. 12

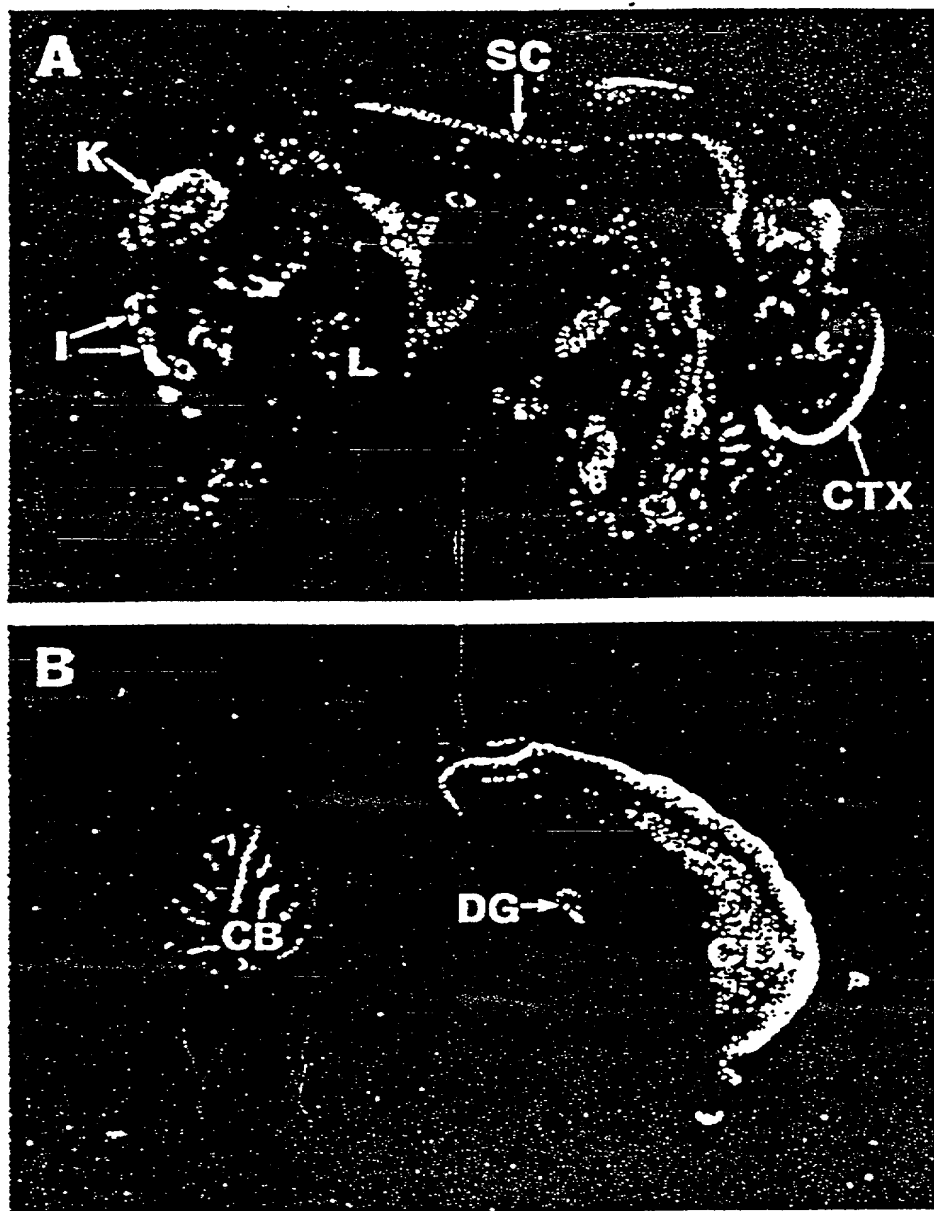


FIG. 13

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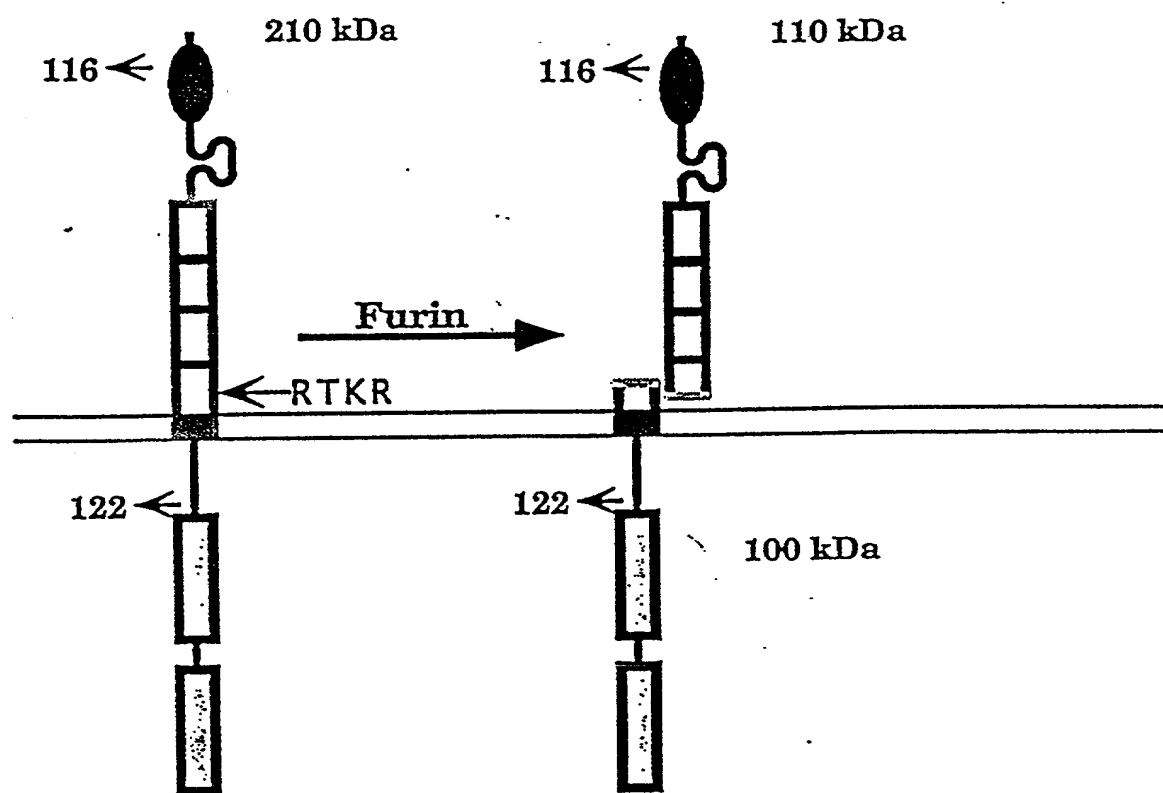


FIG. 14

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1	ATGGATACGACTGCGGCGGCGCGCTGCCTGCTTTTGTGGCGCTCTTGCTCCTCTCTCCTTGGCCTCTCCTGGGATCGGC	80
1	M D T T A A A A L P A F V A L L L L S P W P L L G S A	27
81	CCAAGGCCAGTTCTCCGAGGTGGCTGTACTTTTGATGATGGTCCAGGGGCTGTGATTACCACCAGGATCTGTATGATG	160
27	Q G Q F S A G G C T F D D G P G A C D Y H Q D L Y D D	53
161	ACTTTGAATGGGTGCATGTTAGTGCTCAAGAGCCTCATTATCTACCACCCGAGATGCCCAAGGTTCTATATGATAGTG	240
54	F E W V H V S A Q E P H Y L P P E M P Q G S Y M I V	80
241	GACTCTTCAGATCAGACCCCTGGAGAAAAAGCCAGACTTCAGCTGCCTACAATGAAGGAGAACGACACTCACTGCATTGA	320
81	D S S D H D P G E K A R L Q L P T M K E N D T H C I D	107
321	TTTCAGTTACCTATTATATAGCCAGAAAGGACTGAATCCTGGCACTTTGAACATATTAGTTAGGGTGAATAAAGGACCTC	400
107	F S Y L L Y S Q K G L N P G T L N I L V R V N K G P L	133
401	TTGCCAATCCAATTGGAATGTGACTGGATTACGGGTAGAGATTGGGCTTCGGGCTGAGCTAGCAGTGAGCACCTTTTGG	480
134	A N P I W N V T G F T G R D W L R A E L A V S T F W	160
481	CCCAATGAATATCAGGTAATATTGAAGCTGAAGTCTCAGGAGGGAGAAGTGTTATATTGCCATTGATGACATCCAAGT	560
161	P N E Y Q V I F E A E V S G G R S G Y I A I D D I Q V	187
561	ACTGAGTTATCCTTGTGATAAATCTCCTCATTCTCCTCCGCTCTAGGGGATGTAGAGGTGAATGCAGGGCAAAACGCTACAT	640
187	L S Y P C D K S P H F L R L G D V E V N A G Q N A T F	213
641	TTCAGTGCAATTGCCACAGGGAGAGATGCTGTGCATAACAAGTTATGGCTCCAGAGACGAAATGGAGAAGATATACCAGTA	720
214	Q C I A T G R D A V H N K L W L Q R R N G E D I P V	240
721	GCCCAGACTAAGAACATCAATCATAGAAGGTTTGGCGCTTCCTTCAGATTGCAAGAAGTGACAAAACTGACCAGGATTT	800
241	A Q T K N I N H R R F A A S F R L Q E V T K T D Q D L	267
801	GTCCTGCTGTGTAAGTCACTCAGTCAAGAGGTTCCGGTGTGTCCAATTTTGCTCAACTTATTGTGAGAGAACCGCCAAGAC	880
267	Y R C V T Q S E R G S G V S N F A Q L I V R E P P R P	293
881	CCATTGCTCCTCCTCAGCTTCTTGGTGTGGGCTACATATTTGCTGATCCAACTAAATGCCAACTCGATCATTTGGCGAT	960
294	I A P P Q L L G V G P T Y L L I Q L N A N S I I G D	320
961	GGTCCTATCATCTGAAAGAAGTAGAGTACCGAATGACATCAGGATCCCTGGACAGAAACCCATGCAGTCAATGCTCCAAC	1040
321	G P I I L K E V E Y R M T S G S W T E T H A V N A P T	347
1041	TTACAAATTTATGGCATTATAGATCCAGATACCGAATATGAGATCCGAGTTCTACTTACAAGACCTGGTGAAGGTGGAACGG	1120
347	Y K L W H L D P D T E Y E I R V L L T R P G E G G T G	373
1121	GGCTCCCAGGACCTCCACTAATCACCAGAACAAATGTGCAGAACCTATGAGAACCCCAAGACATTAAAGATTGCTGAA	1200
374	L P G P P L I T R T K C A E P M R T P K T L K I A E	400
1201	ATACAGGCAAGACGGATTGCTGTGGACTGGGAATCTTGGGTTACAACATTACGCGTTGCCACACTTTTAAATGTCACTAT	1280
401	I Q A R R I A V D W E S L G Y N I T R C H T F N V T I	427
1281	CTGCTACCATTTACTTCCGTGGTCACAACGAGAGCAAGGCAGACTGTTTGGACATGGACCCCAAGCCCTCAGCATGTTG	1360
427	C Y H Y F R G H N E S K A D C L D M D P K A P Q H V V	453
1361	TGAACCATCTGCCACCTTATACAAATGTCAGCCTCAAGATGATCCTAACCAATCCAGAGGGAAGGAAGGAGAGTGAAGAG	1440
454	N H L P P Y T N V S L K M I L T N P E G R K E S E E	480
1441	ACAATTATTCAAAGTGAAGATGTGCCTGGTCCCGTACCAGTAAAATCTCTTCAAGGAACATCCTTTGAAAAATAAGAT	1520
481	T I I Q T D E D V P G P V P V K S L Q G T S F E N K I	507
1521	CTTCTTGAAGTGAAGAAACCTTTGGATCCAAATGGAATCATCACTCAATATGAGATCAGCTATAGCAGTATAAGATCAT	1600
507	F L N W K E P L D P N G I I T Q Y E I S Y S S I R S F	533
1601	TTGATCCTGCAGTCCCAAGTGGCTGGACCTCCCAGACTGTATCAAAATTTATGGAACAGTACACACCATGTCTTTATGCAT	1680
534	D P A V P V A G P P Q T V S N L W N S T H H V F M H	560
1681	CTCCACCCTGGAACACGTACCAGTTTTCATAAGAGCCAGCACGGTCAAAGGCTTTGGTCCAGCCACAGCCATCAATGT	1760
561	L H P G T T Y Q F F I R A S T V K G F G P A T A I N V	587
1761	CACCACCAATATCTCAGCTCCAACTTTACCTGACTATGAAGGAGTTGATGCCTCTCTCAATGAAACTGCCACCACAATAA	1840
587	T T N I S A P T L P D Y E G V D A S L N E T A T T I T	613
1841	CTGTATTGTTGAGACCAGCACAAAGGCTGCTCCTATCAGTGCTTATCAGATTGTTGTGGAAGAAGTGCACCCACAC	1920
614	V L L R P A Q A K G A P I S A Y Q I V V E E L H P H	640

FIG. 15(1)

3841	GGCTGCCCTCAGTACTGGCCAGAGGAAGGGATGCTACGATATGGCCCCATCCAAGTGAATGTATGTCTTGTTCATGGA	3920
1281	G C P Q Y W P E E G M L R Y G P I Q V E C M S C S M D	1307
3921	CTGTGATGTGATCAACCGGATTTTTAGGATATGCAATCTAACAAGACCACAGGAAGGTTATCTGATGGTGCACAGTTTC	4000
1307	C D V I N R I F R I C N L T R P Q E G Y L M V Q Q F Q	1333
4001	AGTACCTAGGATGGGCTTCTCATCGAGAAGTGCTGGATCCAAAAGGTCATTCTTGAAACTGATACTTCAGGTGAAAAAG	4080
1334	Y L G W A S H R E V P G S K R S F L K L I L Q V E K	1360
4081	TGGCAGGAGGAATGCGAGGAAGGGGAAGGCCGGACGATTATCCACTGCCTAAATGGTGGCGGGCGAAGTGGCATGTTCTG	4160
1361	W Q E E C E E G E G R T I I H C L N G G G R S G M F C	1387
4161	TGCTATAGGCATCGTGTGTTGAAATGGTGAAACGGCAAATGTTGTGATGTTTTCCATGCAGTAAAGACACTGAGGAACA	4240
1387	A I G I V V E M V K R Q N V V D V F H A V K T L R N S	1413
4241	GCAAGCCAAACATGGTGGAAAGCCCCGGAGCAATACCGTTTCTGCTATGATGTAGCTTTGGAGTACCTGGAATCATCTTAG	4320
1414	K P N M V E A P E Q Y R F C Y D V A L E Y L E S S *	1439
4321	TTGGGTGAGACTCTTTAAAGTGATCCATGAAGAAACCTGTCCATCTATTGAGCCAGCAGCTGTTGTACCTGTACACTT	4400
4401	GTGCAGAAAGATTTTAATGTTGGGGGTGGGAGACTTTTACATTTGAGAGGTAAGTATTTTTTTTATGAAGTTGTGTAT	4480
4481	CTTAATAAAAAGAACTGAATAGTTTTTATTACTATATTAAAGCATCAACATTTTCATGCCACATAAAATTATATTAAATA	4560
4561	AGAACCAGATTTGAAATGGAACAGTATTGGTGTGTTGTACAGTGAACATGCCACCTTTTTCCATGGTTTCAGGTAGTGCAGC	4640
4641	TACCACATGTT. 4651	

(SEQ ID NO: 2)

FIG. 15 (3)

09007669 "100101"

MCP7	MDTTAAALPAPVALLLLSPWELLSSAQCF	SAGGCTFDDGFGACDYHQLDYDDFENVHVSAQEPHYLPFENPCGSGYHIV	80
hrPTM	-MR LGTC - TL G -----TAAGET -	L EPIST G S SEG N EQ NTLTKPTSD W S L L	71
MCP7	DSSDHDPEKARLQLPTMKENDTHCIDFSTLLYSQGLNPGTLNILVRVNGKPLANPIWNTGFTGRDWLRAELAVSTFW		160
hrPTM	NA GRPE QR H L QL	H FVS KNSP L VY K N G IS DPT T N I	151
MCP7	FNEYQVIFEAEVSGGRSGYLAIDDIQVLSYPCDRSPHPLRLGOVEVNAGQATQC IATGRDAVHNKLWLQRRNGEDIPV		240
hrPTM	F V-ITS HQ L EVK GH THT	IGN F S I TVAGER GIDVR A L	230
MCP7	AQTKNINHRFAASPRLCVTKTDQDLRCVTQSERGSGVSNFAQLIVREPPREIAPPQLLGVGPTYLLIQINANSIIGD		320
hrPTM	KEI VTSS I NVVNT R AGK MIRT G V I Y E V K V	AS A W N	310
MCP7	GPILLKEVEYRMTSGSWTETHAVNAPTXYKLWHLDPDTEYEIRVLLTRGEGGTGLPGPPLITRTKCAEPMRTPKTLKIAE		400
hrPTM	VAR CTA NDRQP DSTS IG	S S A R D G R K EVV	390
MCP7	IQARRIAVDWESLGYNTIRCHTFNVTICYHYPRGHE--SKADCLDMDKPAQHVVNHLFPYTNVSLKMITNPEGRKES		478
hrPTM	VKS Q TIR ET V SY L VH C QV QQ QVREESW TENGH	TITN S V L M	470
MCP7	EETIIQTDDEVDGPFVVKSLQGTSEFNKIPLNWKEPLDPNGILITQYEISYSSIRSFDPAPVPVAGPEQTVSNLWNSTHVF		558
hrPTM	Q L V L A TE I ST E Q R TQTY V L T KAVS	EIDLSNQSGR K G E FL	550
MCP7	MHLRPGTTYQFFIRASTVKGFGPATAINVITINISAPTLDPDYEGVDASINETATTITVLLRPAQAKGAPISAYQIVVEELH		638
hrPTM	FG Y S T A PATNQF K SM A -LETP Q DN V M K HSR V V	ER	629
MCP7	PHRTKREAGAMECYQVFPVYQNAMSGGAPYFAALEPFGNLFEPAPFTVGDNRITYQGFNAPPLAPRKGYNIYQAMSSVE		718
hrPTM	R KTEILK P IEF SLINSQ	P ADS QAAQ I K N Y T L Y S R A RAN	709
MCP7	KETKTQCVRIATKAATEEVEVIPDEAKQTRVVKLAGISAGILVFILLLVVILIVKSKLAKKRRDAGNTRQEMTHV		798
hrPTM	G ID QV G A-T KPV EE ET VI L VIIIF G V VM R	ET SS V	788
MCP7	NAMDRSYADQSTLHAEDELSITFMDQRNFSRY-----ENHSATAESSRLLDWPRY-LGE		852
hrPTM	S K E G -NCDEAP -- T LNC SVSSSSPTMKNTLSTSVPNSTYPD T THASDT S VQSH T KKR		865
MCP7	GTESPYTQGLHPAIRVADLLQRIINLHKTSDSYGPKEEYESFFEGQSASWDVAKKDONRAKNRYGNIIAYDESRVILQV		932
hrPTM	PADV	TQ CAEG P S E M R TI	945
MCP7	EDDPSSDYINANYIDGYQRFSEHYIATQGFVHETVYDFWRHINQEQSACIVMVTNLVEVGRVKCYKWPDDTEVYGDPKVT		1012
hrPTM	G TN G H N MQ I V H NT S I	C I K I	1025
MCP7	CVEMEPLAEYVVRTFTLERRGYNEIREVKQPHPTGMPDHGVPHATGILLSFIRRVKLSNPPSAGPIVVECSAGAGRTGCY		1092
hrPTM	LI T L I AV K VH IR	G V Q SKS L E	1105
MCP7	IVIDIMLDMAREGVVDIYNCVKALRSRRINMVQTEQYIFHDAILEACLCGETAIPVCEPKAAYPDMIRIDSQTNSSH		1172
hrPTM	RE V V	D SV ASQVRS L Y NKL P Q	1185
MCP7	LKDEFQTLNSVTPRLQAEDCSIACLPRNHKRNRFMIMLPFDRCLPFLITIDGESSNYINAALMDSTROPAAETVQYELP		1252
hrPTM	I E R M T RV	L E C I K S H	1265
MCP7	NTVKDFWRLVYDYGCTSIIVMLNEVDLSQGCQYWPBEGMLRYGPIQVECMSCSMDCDVIDIRIFRICNLTRPOSGYLMVQ		1332
hrPTM	L E V D : PA L N VH H	FV ADLEE I S Y AA D R	1345
MCP7	FQYLGAWSHREVPGSKRSPKLILQVEKWOEECEBEGGRTIIHCLNGGGRSGMCAIGIVVEMVKRONVVDVFAVKTLR		1412
hrPTM	F PMY DT V R D YNG P VV	T S C LRH RT	1425
MCP7	NSKPNMWEAPEQYRFQYDALEYLESS*		1439
hrPTM	N DLLD K E N G*		1452

FIG. 16

00887669 100101

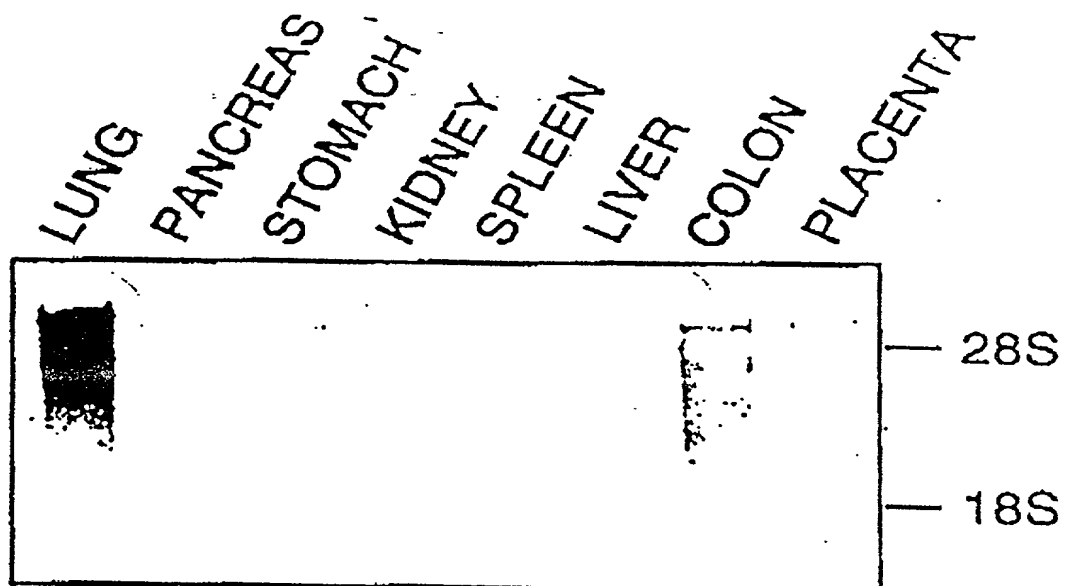


FIG. 17

TOPDOT 69978860

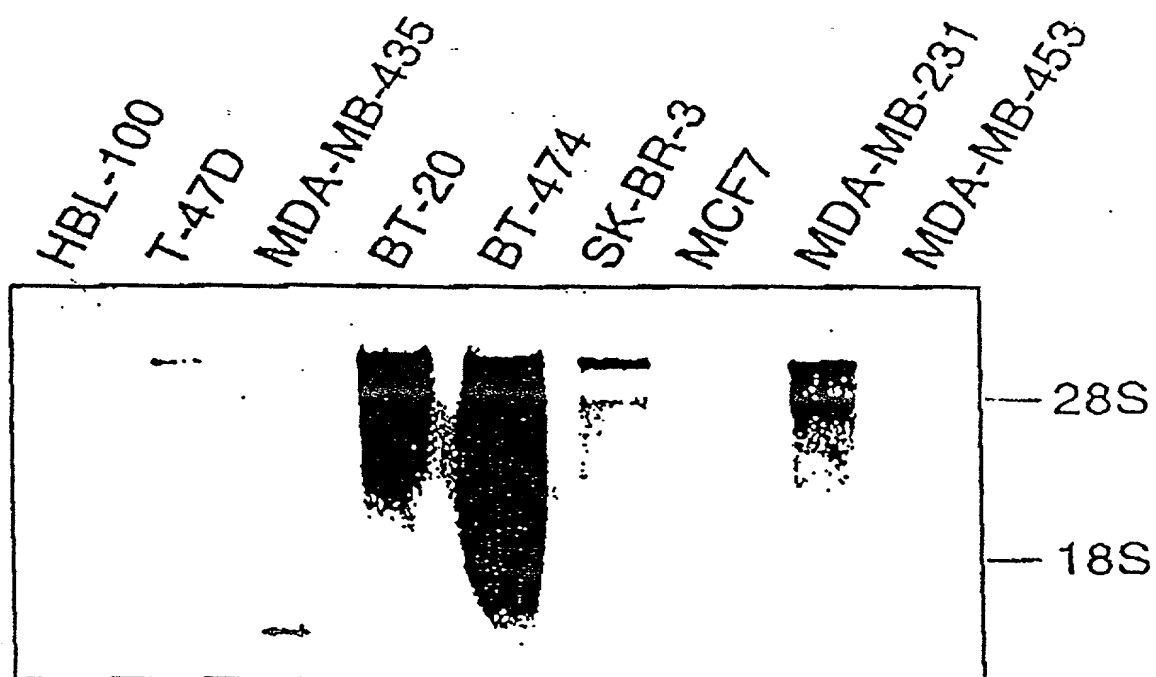


FIG. 18

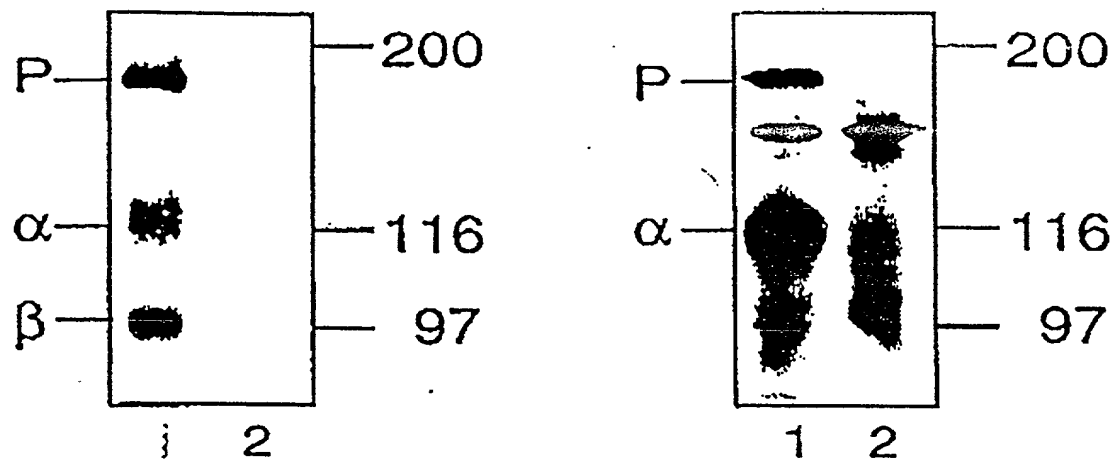


FIG. 19

09887569-100101

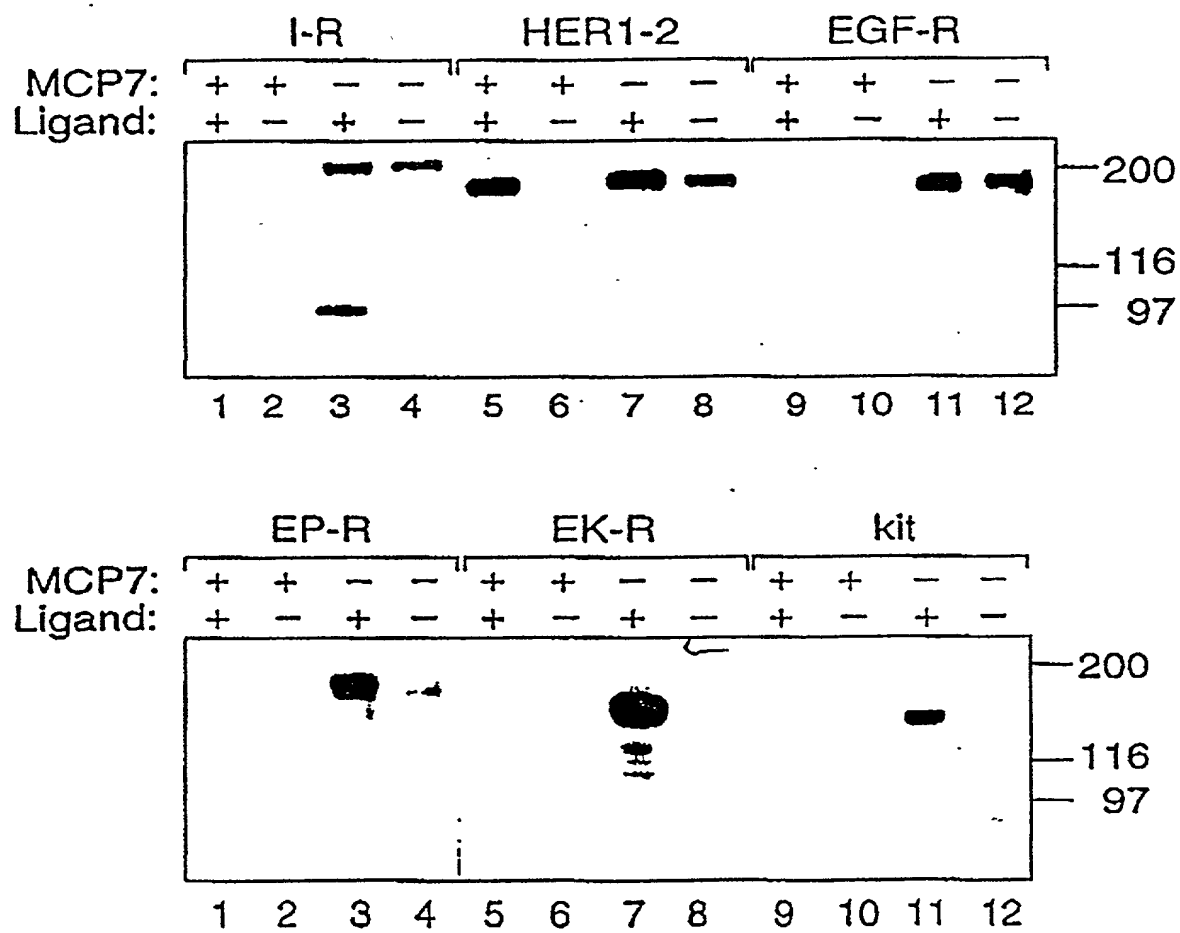


FIG. 20

09887669-100101

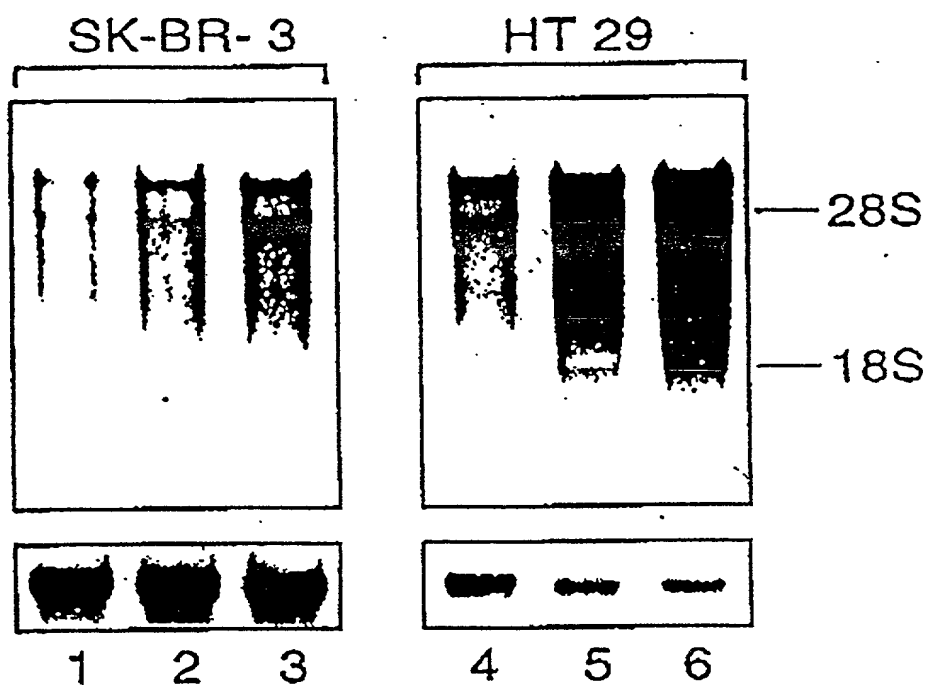


FIG. 21

1 2 3 4 5

190 —
125 —
88 —
65 —
56 —

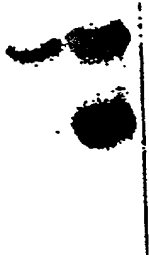
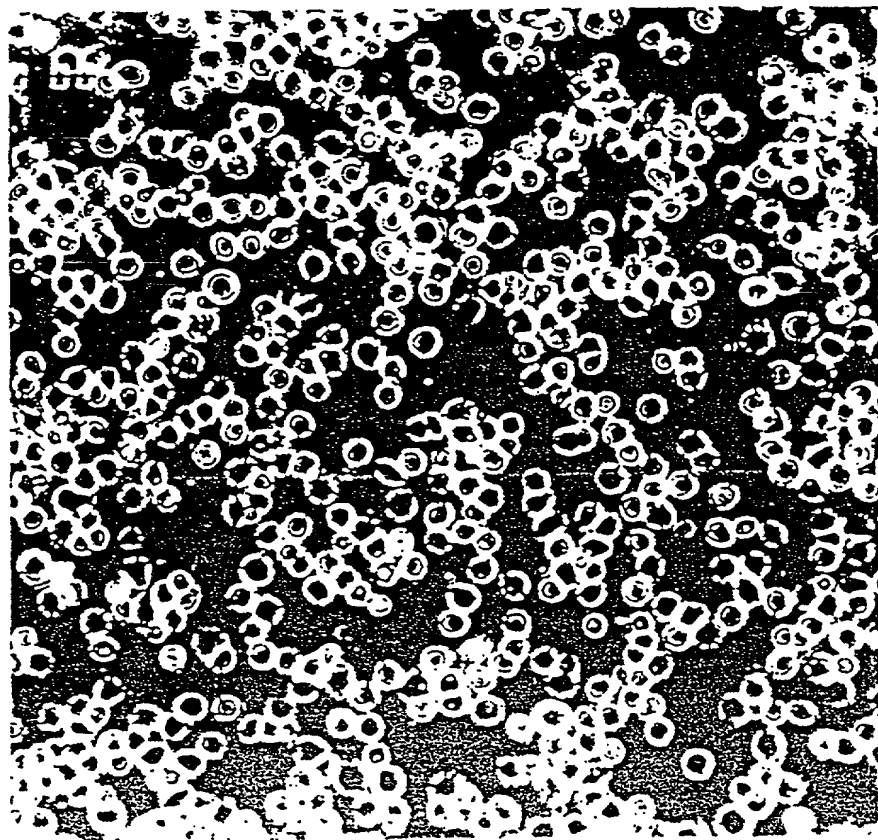


FIG. 22 A

FOOTNOT "699/8860

Control



R-PTP-K

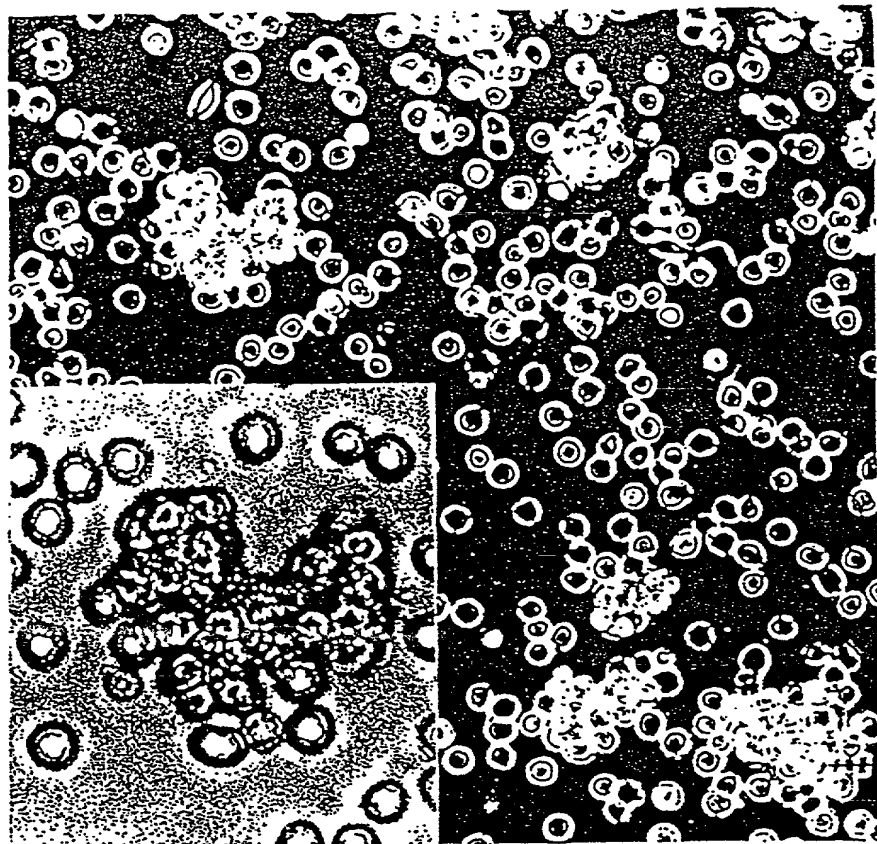


FIG. 22B

Time (Hours)	100% 100% (●)	100% 50% (○)	50% 50% (◇)
0:00	2100	1800	1300
0:30	4600	2100	1900
1:00	5600	3200	2400
1:30	6200	4300	2100
2:00	7800	3300	2600
3:00	7300	3400	1900

1000

FIG. 22D

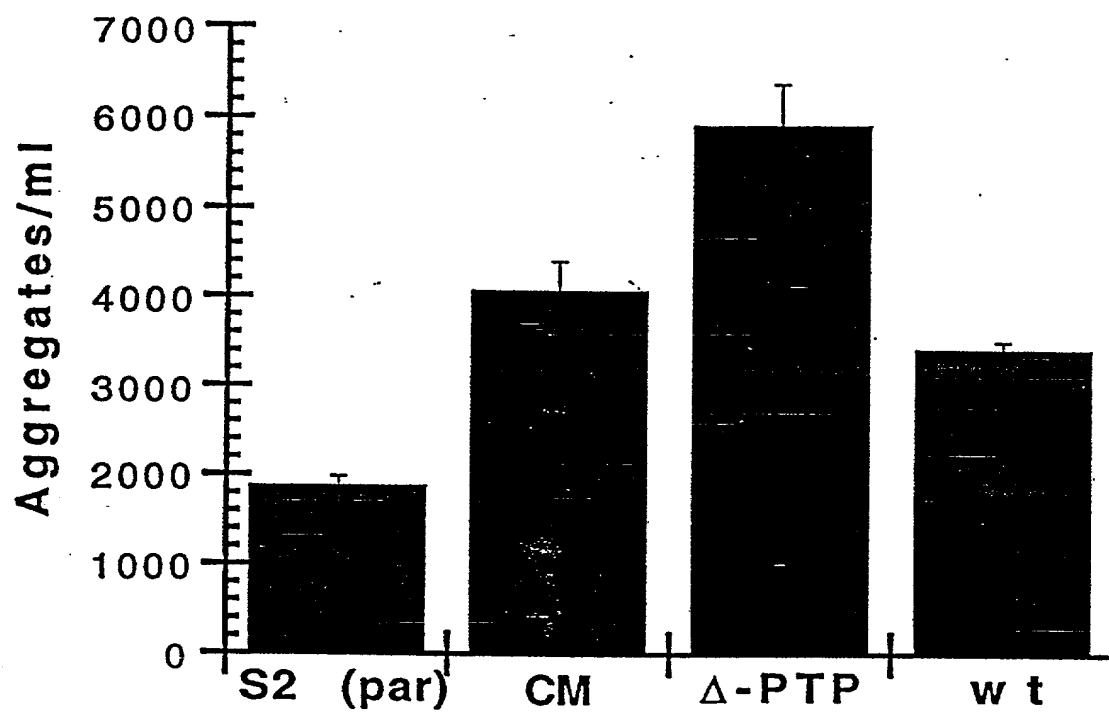
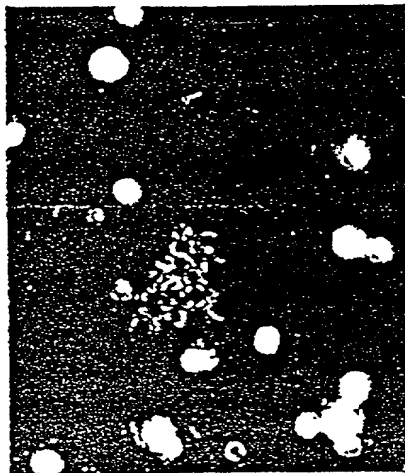


FIG. 22D

$\kappa^-(\text{dil}) + \kappa^+$



$\kappa^- + \kappa^+(\text{dil})$



$\kappa^+ + \kappa^+(\text{dil})$

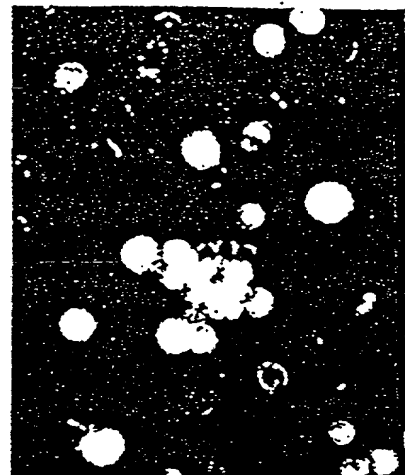


FIG. 23

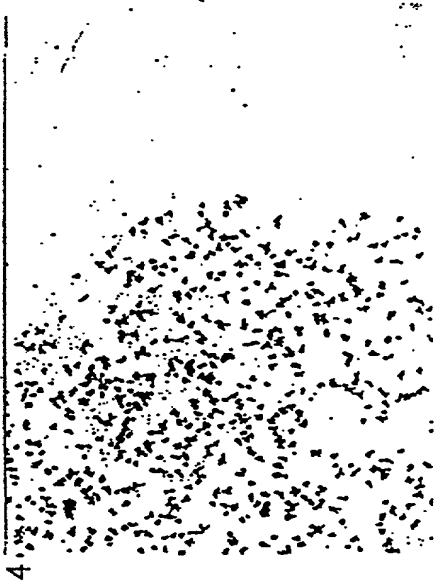
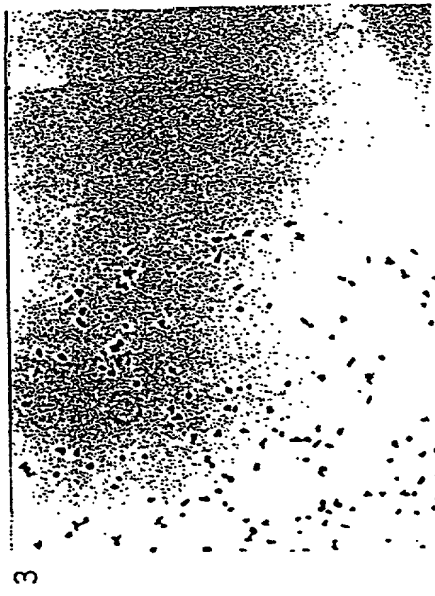
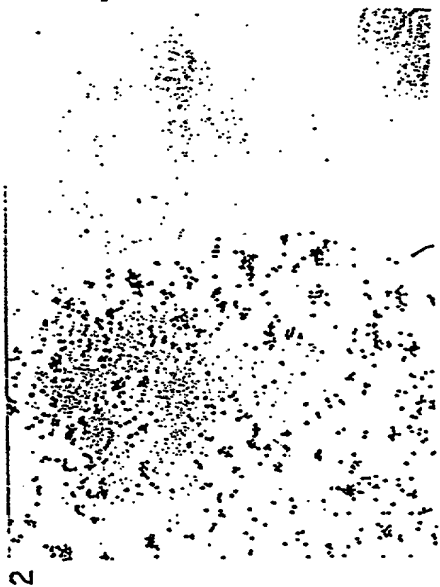
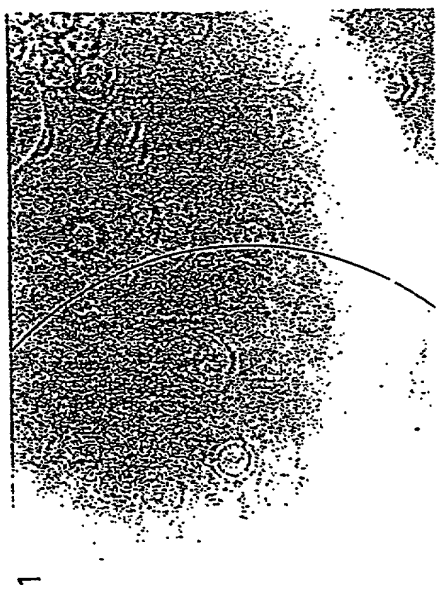


FIG. 24